

CRF Errors Corrected by the STIC Systems Branch

CRF Processing Date: 1/31/2002
Edited by: A
Verified by: A (STIC Staff)OPE 0890
0231

ENTERED

Serial Numbr: 09/970,616

Changed a file from non-ASCII to ASCII

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

Edited a format error in the Current Application Data section, specifically:

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other _____

Added the mandatory heading and subheadings for "Current Application Data".

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

Inserted colons after headings/subheadings. Headings edited included: CITY; STATE

Deleted extra, invalid, headings used by an applicant, specifically:

Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file; page numbers throughout text; other invalid text, such as _____

Inserted mandatory headings, specifically:

Corrected an obvious error in the response, specifically:

Edited identifiers where upper case is used but lower case is required, or vice versa.

Corrected an error in the Number of Sequences field, specifically:

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

Other: _____



OIPE

RAW SEQUENCE LISTING DATE: 01/31/2002
 PATENT APPLICATION: US/09/970,616 TIME: 20:30:35

Input Set : A:\PTO.AMC.txt
 Output Set: N:\CRF3\01312002\I970616.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: SOUPPE, Jerome

7 BEUDEKER, Robert Franciscus

9 (ii) TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF
 10 ALCOHOLIC BEVERAGES USING MALTSEED

12 (iii) NUMBER OF SEQUENCES: 8

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: LADAS & PARRY
 16 (B) STREET: 26 WEST 61 STREET

17 (C) CITY: NEW YORK

18 (D) STATE: NY

19 (E) COUNTRY: USA

20 (F) ZIP: 10023

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: Microsoft Windows for Workgroups

26 (D) SOFTWARE: WordPerecet 8

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/970,616

C--> 30 (B) FILING DATE: 04-Oct-2001

31 (C) CLASSIFICATION: 435

C--> 41 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: 09/230,590

35 (B) FILING DATE: 28-APR-1999

38 (A) APPLICATION NUMBER: PCT/EP97/04016

39 (B) FILING DATE: 23-JUL-1997

42 (A) APPLICATION NUMBER: EP 96202195.2

43 (B) FILING DATE: 05-AUG-1996

45 (viii) ATTORNEY/AGENT INFORMATION:

46 (A) NAME: MASS, CLIFFORD J.

C--> 47 (B) REGISTRATION NUMBER:

48 (C) REF./DOCKET NO.: U-012094-9

50 (ix) TELECOMMUNICATION INFORMATION:

C--> 53 (A) TELEPHONE: 233288

55 (2) INFORMATION FOR SEQ ID NO: 1:

57 (i) SEQUENCE CHARACTERISTICS:

58 (A) LENGTH: 557 base pairs

59 (B) TYPE: nucleic acid

60 (C) STRANDEDNESS: double

61 (D) TOPOLOGY: linear

63 (ii) MOLECULE TYPE: cDNA

RAW SEQUENCE LISTING

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65 (iii) HYPOTHETICAL: NO
 C--> 67 (iv) ANTI-SENSE: NO
 69 (ix) FEATURE:
 70 (A) NAME/KEY: CDS
 71 (B) LOCATION: 1..555
 72 (D) OTHER INFORMATION: /product= "mature protein"
 74 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 76 ATG AGC GCG GGA ATC AAC TAC GTC CAG AAC TAC AAT GGC AAC CTC GGC 48
 77 Met Ser Ala Gly Ile Asn Tyr Val Gln Asn Tyr Asn Gly Asn Leu Gly
 78 1 5 10 15
 80 GAC TTT ACT TAC GAC GAG TCA GCG GGA ACT TTC AGC ATG TAT TGG GAG 96
 81 Asp Phe Thr Tyr Asp Glu Ser Ala Gly Thr Phe Ser Met Tyr Trp Glu
 82 20 25 30
 84 GAT GGC GTG TCC TCA GAC TTC GTC GTG GGA CTG GGC TGG ACC ACT GGA 144
 85 Asp Gly Val Ser Ser Asp Phe Val Val Gly Leu Gly Trp Thr Thr Gly
 86 35 40 45
 88 TCA TCC AAT GCG ATC ACC TAC AGC GCC GAG TAC TCC GCG TCA GGA TCA 192
 89 Ser Ser Asn Ala Ile Thr Tyr Ser Ala Glu Tyr Ser Ala Ser Gly Ser
 90 50 55 60
 92 GCC TCC TAT CTG GCC GTG TAC GGA TGG GTG AAC TAC CCG CAG GCC GAG 240
 93 Ala Ser Tyr Leu Ala Val Tyr Gly Trp Val Asn Tyr Pro Gln Ala Glu
 94 65 70 75 80
 96 TAC TAC ATC GTG GAG GAT TAC GGA GAT TAC AAC CCA TGC AGC TCA GCG 288
 97 Tyr Tyr Ile Val Glu Asp Tyr Gly Asp Tyr Asn Pro Cys Ser Ser Ala
 98 85 90 95
 100 ACC TCC CTC GGA ACT GTG TAC AGC GAC GGC TCC ACC TAC CAG GTC TGC 336
 101 Thr Ser Leu Gly Thr Val Tyr Ser Asp Gly Ser Thr Tyr Gln Val Cys
 102 100 105 110
 104 ACC GAC ACC CGC ACT AAC GAG CCG TCA ATC ACC GGC ACT TCC ACC TTC 384
 105 Thr Asp Thr Arg Thr Asn Glu Pro Ser Ile Thr Gly Thr Ser Thr Phe
 106 115 120 125
 109 ACC CAG TAC TTC AGC GTG CGC GAG TCC ACT CGC ACC TCA GGA ACC GTG 432
 110 Thr Gln Tyr Phe Ser Val Arg Glu Ser Thr Arg Thr Ser Gly Thr Val
 111 130 135 140
 113 ACC GTC GCG AAC CAC TTC AAC TTC TGG GCG CAG CAC GGA TTC GGC AAC 480
 114 Thr Val Ala Asn His Phe Asn Phe Trp Ala Gln His Gly Phe Gly Asn
 115 145 150 155 160
 117 AGC GAC TTT AAC TAC CAG GTG GTC GCA GTG GAG GCA TGG TCA GGA GCG 528
 118 Ser Asp Phe Asn Tyr Gln Val Val Ala Val Glu Ala Trp Ser Gly Ala
 119 165 170 175
 121 GGC TCA GCG TCC GTC ACT ATC AGC TCC TG 557
 122 Gly Ser Ala Ser Val Thr Ile Ser Ser
 123 180 185
 126 (2) INFORMATION FOR SEQ ID NO: 2:
 128 (i) SEQUENCE CHARACTERISTICS:
 129 (A) LENGTH: 185 amino acids
 130 (B) TYPE: amino acid
 131 (D) TOPOLOGY: linear
 133 (ii) MOLECULE TYPE: protein

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135 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 137 Met Ser Ala Gly Ile Asn Tyr Val Gln Asn Tyr Asn Gly Asn Leu Gly
 138 1 5 10 15
 140 Asp Phe Thr Tyr Asp Glu Ser Ala Gly Thr Phe Ser Met Tyr Trp Glu
 141 20 25 30
 143 Asp Gly Val Ser Ser Asp Phe Val Val Gly Leu Gly Trp Thr Thr Gly
 144 35 40 45
 146 Ser Ser Asn Ala Ile Thr Tyr Ser Ala Glu Tyr Ser Ala Ser Gly Ser
 147 50 55 60
 149 Ala Ser Tyr Leu Ala Val Tyr Gly Trp Val Asn Tyr Pro Gln Ala Glu
 150 65 70 75 80
 152 Tyr Tyr Ile Val Glu Asp Tyr Gly Asp Tyr Asn Pro Cys Ser Ser Ala
 153 85 90 95
 155 Thr Ser Leu Gly Thr Val Tyr Ser Asp Gly Ser Thr Tyr Gln Val Cys
 156 100 105 110
 158 Thr Asp Thr Arg Thr Asn Glu Pro Ser Ile Thr Gly Thr Ser Thr Phe
 159 115 120 125
 161 Thr Gln Tyr Phe Ser Val Arg Glu Ser Thr Arg Thr Ser Gly Thr Val
 162 130 135 140
 164 Thr Val Ala Asn His Phe Asn Phe Trp Ala Gln His Gly Phe Gly Asn
 165 145 150 155 160
 167 Ser Asp Phe Asn Tyr Gln Val Val Ala Val Glu Ala Trp Ser Gly Ala
 168 165 170 175
 170 Gly Ser Ala Ser Val Thr Ile Ser Ser
 171 180 185
 174 (2) INFORMATION FOR SEQ ID NO: 3:
 176 (i) SEQUENCE CHARACTERISTICS:
 177 (A) LENGTH: 71 base pairs
 178 (B) TYPE: nucleic acid
 179 (C) STRANDEDNESS: single
 180 (D) TOPOLOGY: linear
 182 (ii) MOLECULE TYPE: cDNA
 184 (iii) HYPOTHETICAL: NO
 C--> 186 (iv) ANTI-SENSE: NO
 188 (vi) ORIGINAL SOURCE:
 189 (A) ORGANISM: Nicotiana tabacum
 191 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 193 AACTCCCTCA AGAGCTTCCC CTTTTATGCC TTCCCTTGTT TTGGCCAATA CTTTGTAGCT 60
 195 GTTACGCATG C 71
 198 (2) INFORMATION FOR SEQ ID NO: 4:
 200 (i) SEQUENCE CHARACTERISTICS:
 201 (A) LENGTH: 80 base pairs
 202 (B) TYPE: nucleic acid
 203 (C) STRANDEDNESS: single
 204 (D) TOPOLOGY: linear
 206 (ii) MOLECULE TYPE: cDNA
 208 (iii) HYPOTHETICAL: NO
 C--> 210 (iv) ANTI-SENSE: YES
 212 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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214 CCATGGCATG CGTAACAGCT ACAAAAGTATT GGCCAAAACA AAGGAAGGCA TAAAAGGGGA      60
215 AGCTCTGAG GAAGTTCATG      80
219 (2) INFORMATION FOR SEQ ID NO: 5:
221     (i) SEQUENCE CHARACTERISTICS:
222         (A) LENGTH: 21 base pairs
223         (B) TYPE: nucleic acid
224         (C) STRANDEDNESS: single
225         (D) TOPOLOGY: linear
227     (ii) MOLECULE TYPE: cDNA
229     (iii) HYPOTHETICAL: NO
C--> 231     (iv) ANTI-SENSE: NO
233     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
235 ATGGATGGCA TGCTGTTGTA G      21
238 (2) INFORMATION FOR SEQ ID NO: 6:
240     (i) SEQUENCE CHARACTERISTICS:
241         (A) LENGTH: 21 base pairs
242         (B) TYPE: nucleic acid
243         (C) STRANDEDNESS: single
244         (D) TOPOLOGY: linear
246     (ii) MOLECULE TYPE: cDNA
248     (iii) HYPOTHETICAL: NO
C--> 250     (iv) ANTI-SENSE: NO
252     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
254 GCACAATTCT CGAGGAGACC G      21
257 (2) INFORMATION FOR SEQ ID NO: 7:
259     (i) SEQUENCE CHARACTERISTICS:
260         (A) LENGTH: 21 base pairs
261         (B) TYPE: nucleic acid
262         (C) STRANDEDNESS: single
263         (D) TOPOLOGY: linear
265     (ii) MOLECULE TYPE: cDNA
267     (iii) HYPOTHETICAL: NO
C--> 269     (iv) ANTI-SENSE: NO
271     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
273 CCTCTTAAGG ATCCAATGCG G      21
276 (2) INFORMATION FOR SEQ ID NO: 8:
278     (i) SEQUENCE CHARACTERISTICS:
279         (A) LENGTH: 21 base pairs
280         (B) TYPE: nucleic acid
281         (C) STRANDEDNESS: single
282         (D) TOPOLOGY: linear
284     (ii) MOLECULE TYPE: cDNA
286     (iii) HYPOTHETICAL: NO
C--> 288     (iv) ANTI-SENSE: NO
290     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
292 CTTATCTGAA TTCCGAAGCT C      21

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/970,616

DATE: 01/31/2002

TIME: 20:30:36

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\01312002\I970616.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:33 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:41 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:47 M:220 C: Keyword misspelled or invalid format, [(B) REGISTRATION NUMBER:]
L:47 M:220 C: Keyword misspelled or invalid format, Poss data loss, (B) REGISTRATION NUMBER:
L:51 M:220 C: Keyword misspelled or invalid format, [(A) TELEPHONE:]
L:52 M:220 C: Keyword misspelled or invalid format, [(A) TELEPHONE:]
L:53 M:220 C: Keyword misspelled or invalid format, [(A) TELEPHONE:]
L:67 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:186 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:210 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:231 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:250 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:269 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:288 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]